

0590

1204

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/842,256

DATE: 12/17/2001

TIME: 14:43:16

Input Set : N:\Crif3\RULE60\09842256.txt

Output Set: N:\CRF3\12172001\I842256.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Chambon, Pierre
 7 Gronemeyer, Hinrich
 8 Voegel, Johannes
 9 Lutz, Yves

ENTERED

LIMITED

11 (ii) TITLE OF INVENTION: Transcriptional Intermediary Factor-2

13 (iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

17 (B) STREET: 1100 New York Avenue, NW, Suite 600

18 (C) CITY: Washington

19 (D) STATE: DC

20 (E) COUNTRY: USA

21 (F) ZIP: 20005-3934

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/842,256

C--> 31 (B) FILING DATE: 26-Apr-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 08/891,640

36 (B) FILING DATE:

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Steffe, Eric K.

40 (B) REGISTRATION NUMBER: 36,688

41 (C) REFERENCE/DOCKET NUMBER: 1383.0130001/EKS

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 202-371-2600

45 (B) TELEFAX: 202-371-2540

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 6156 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: double

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

59 (ix) FEATURE:

60 (A) NAME/KEY: CDS

61 (B) LOCATION: 163..4554

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

66 GGCGGCCGCA GCCTTCGGCTA CAGCTTCGGC GGCGAAGGTC AGCGCCGACG GCAGCCGGCA 60
 68 CCTGACGGCG TGACCGACCC GAGCCGATTT CTCTTGATT TGGCTACACA CTTATAGATC 120

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70 TTCTGCACTG TTTACAGGCA CAGTTGCTGA TATGTGTTCA AG ATG AGT GGG ATG      174
71                                     Met Ser Gly Met
72                                     1
74 GGA GAA AAT ACC TCT GAC CCC TCC AGG GCA GAG ACA AGA AAG CGC AAG      222
75 Gly Glu Asn Thr Ser Asp Pro Ser Arg Ala Glu Thr Arg Lys Arg Lys
76   5          10          15          20
78 GAA TGT CCT GAC CAA CTT GGA CCC AGC CCC AAA AGG AAC ACT GAA AAA      270
79 Glu Cys Pro Asp Gln Leu Gly Pro Ser Pro Lys Arg Asn Thr Glu Lys
80          25          30          35
82 CGT AAT CGT GAA CAG GAA AAT AAA TAT ATA GAA GAA CTT GCA GAG TTG      318
83 Arg Asn Arg Glu Gln Glu Asn Lys Tyr Ile Glu Glu Leu Ala Glu Leu
84          40          45          50
86 ATT TTT GCA AAT TTT AAT GAT ATA GAC AAC TTT AAC TTC AAA CCT GAC      366
87 Ile Phe Ala Asn Phe Asn Asp Ile Asp Asn Phe Asn Phe Lys Pro Asp
88   55          60          65
90 AAA TGT GCA ATC TTA AAA GAA ACT GTG AAG CAA ATT CGT CAG ATC AAA      414
91 Lys Cys Ala Ile Leu Lys Glu Thr Val Lys Gln Ile Arg Gln Ile Lys
92   70          75          80
94 GAA CAA GAG AAA GCA GCA GCT GCC AAC ATA GAT GAA GTG CAG AAG TCA      462
95 Glu Gln Glu Lys Ala Ala Ala Asn Ile Asp Glu Val Gln Lys Ser
96  85          90          95          100
98 GAT GTA TCC TCT ACA GGG CAG GGT GTC ATC GAC AAG GAT GCG CTG GGG      510
99 Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ala Leu Gly
100          105          110          115
102 CCT ATG ATG CTT GAG GCC CTT GAT GGG TTC TTC TTT GTA GTG AAC CTG      558
103 Pro Met Met Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn Leu
104          120          125          130
106 GAA GGC AAC GTT GTG TTT GTG TCA GAG AAT GTG ACA CAG TAT CTA AGG      606
107 Glu Gly Asn Val Val Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Arg
108          135          140          145
110 TAT AAC CAA GAA GAG CTG ATG AAC AAA AGT GTA TAT AGC ATC TTG CAT      654
111 Tyr Asn Gln Glu Glu Leu Met Asn Lys Ser Val Tyr Ser Ile Leu His
112          150          155          160
114 GTT GGG GAC CAC ACG GAA TTT GTC AAA AAC CTG CTG CCA AAG TCT ATA      702
115 Val Gly Asp His Thr Glu Phe Val Lys Asn Leu Leu Pro Lys Ser Ile
116 165          170          175          180
118 GTA AAT GGG GGA TCT TGG TCT GGC GAA CCT CCG AGG CGG AAC AGC CAT      750
119 Val Asn Gly Gly Ser Trp Ser Gly Glu Pro Pro Arg Arg Asn Ser His
120          185          190          195
122 ACC TTC AAT TGT CGG ATG CTG GTA AAA CCT TTA CCT GAT TCA GAA GAG      798
123 Thr Phe Asn Cys Arg Met Leu Val Lys Pro Leu Pro Asp Ser Glu Glu
124          200          205          210
126 GAG GGT CAT GAT AAC CAG GAA GCT CAT CAG AAA TAT GAA ACT ATG CAG      846
127 Glu Gly His Asp Asn Gln Glu Ala His Gln Lys Tyr Glu Thr Met Gln
128          215          220          225
130 TGC TTC GCT GTC TCT CAA CCA AAG TCC ATC AAA GAA GAA GGA GAA GAT      894
131 Cys Phe Ala Val Ser Gln Pro Lys Ser Ile Lys Glu Glu Gly Glu Asp
132          230          235          240
134 TTG CAG TCC TGC TTG ATT TGC GTG GCA AGA AGA GTT CCC ATG AAG GAA      942

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135	Leu	Gln	Ser	Cys	Leu	Ile	Cys	Val	Ala	Arg	Arg	Val	Pro	Met	Lys	Glu	
136	245					250						255				260	
138	AGA	CCA	GTT	CTT	CCC	TCA	TCA	GAA	AGT	TTT	ACT	ACT	CGC	CAG	GAT	CTC	990
139	Arg	Pro	Val	Leu	Pro	Ser	Ser	Glu	Ser	Phe	Thr	Thr	Arg	Gln	Asp	Leu	
140					265					270					275		
142	CAA	GGC	AAG	ATC	ACG	TCT	CTG	GAT	ACC	AGC	ACC	ATG	AGA	GCA	GCC	ATG	1038
143	Gln	Gly	Lys	Ile	Thr	Ser	Leu	Asp	Thr	Ser	Thr	Met	Arg	Ala	Ala	Met	
144					280					285					290		
146	AAA	CCA	GGC	TGG	GAG	GAC	CTG	GTA	AGA	AGG	TGT	ATT	CAG	AAG	TTC	CAT	1086
147	Lys	Pro	Gly	Trp	Glu	Asp	Leu	Val	Arg	Arg	Cys	Ile	Gln	Lys	Phe	His	
148			295							300					305		
150	GCG	CAG	CAT	GAA	GGA	GAA	TCT	GTG	TCC	TAT	GCT	AAG	AGG	CAT	CAT	CAT	1134
151	Ala	Gln	His	Glu	Gly	Glu	Ser	Val	Ser	Tyr	Ala	Lys	Arg	His	His	His	
152		310								315					320		
154	GAA	GTA	CTG	AGA	CAA	GGA	TTG	GCA	TTC	AGT	CAA	ATC	TAT	CGT	TTT	TCC	1182
155	Glu	Val	Leu	Arg	Gln	Gly	Leu	Ala	Phe	Ser	Gln	Ile	Tyr	Arg	Phe	Ser	
156	325					330					335				340		
158	TTG	TCT	GAT	GGC	ACT	CTT	GTT	GCT	GCA	CAA	ACG	AAG	AGC	AAA	CTC	ATC	1230
159	Leu	Ser	Asp	Gly	Thr	Leu	Val	Ala	Ala	Gln	Thr	Lys	Ser	Lys	Leu	Ile	
160					345						350				355		
162	CGT	TCT	CAG	ACT	ACT	AAT	GAA	CCT	CAA	CTT	GTA	ATA	TCT	TTA	CAT	ATG	1278
163	Arg	Ser	Gln	Thr	Thr	Asn	Glu	Pro	Gln	Leu	Val	Ile	Ser	Leu	His	Met	
164					360						365				370		
166	CTT	CAC	AGA	GAG	CAG	AAT	GTG	TGT	GTG	ATG	AAT	CCG	GAT	CTG	ACT	GGA	1326
167	Leu	His	Arg	Glu	Gln	Asn	Val	Cys	Val	Met	Asn	Pro	Asp	Leu	Thr	Gly	
168					375						380				385		
170	CAA	ACG	ATG	GGG	AAG	CCA	CTG	AAT	CCA	ATT	AGC	TCT	AAC	AGC	CCT	GCC	1374
171	Gln	Thr	Met	Gly	Lys	Pro	Leu	Asn	Pro	Ile	Ser	Ser	Asn	Ser	Pro	Ala	
172		390													400		
174	CAT	CAG	GCC	CTG	TGC	AGT	GGG	AAC	CCA	GGT	CAG	GAC	ATG	ACC	CTC	AGT	1422
175	His	Gln	Ala	Leu	Cys	Ser	Gly	Asn	Pro	Gly	Gln	Asp	Met	Thr	Leu	Ser	
176	405					410						415			420		
178	AGC	AAT	ATA	AAT	TTT	CCC	ATA	AAT	GGC	CCA	AAG	GAA	CAA	ATG	GGC	ATG	1470
179	Ser	Asn	Ile	Asn	Phe	Pro	Ile	Asn	Gly	Pro	Lys	Glu	Gln	Met	Gly	Met	
180					425						430				435		
182	CCC	ATG	GGC	AGG	TTT	GGT	GGT	TCT	GGG	GGA	ATG	AAC	CAT	GTG	TCA	GGC	1518
183	Pro	Met	Gly	Arg	Phe	Gly	Gly	Ser	Gly	Gly	Met	Asn	His	Val	Ser	Gly	
184					440						445				450		
186	ATG	CAA	GCA	ACC	ACT	CCT	CAG	GGT	AGT	AAC	TAT	GCA	CTC	AAA	ATG	AAC	1566
187	Met	Gln	Ala	Thr	Thr	Pro	Gln	Gly	Ser	Asn	Tyr	Ala	Leu	Lys	Met	Asn	
188					455						460				465		
190	AGC	CCC	TCA	CAA	AGC	AGC	CCT	GGC	ATG	AAT	CCA	GGA	CAG	CCC	ACC	TCC	1614
191	Ser	Pro	Ser	Gln	Ser	Ser	Pro	Gly	Met	Asn	Pro	Gly	Gln	Pro	Thr	Ser	
192		470													480		
194	ATG	CTT	TCA	CCA	AGG	CAT	CGC	ATG	AGC	CCT	GGA	GTG	GCT	GGC	AGC	CCT	1662
195	Met	Leu	Ser	Pro	Arg	His	Arg	Met	Ser	Pro	Gly	Val	Ala	Gly	Ser	Pro	
196	485					490						495			500		
198	CGA	ATC	CCA	CCC	AGT	CAG	TTT	TCC	CCT	GCA	GGA	AGC	TTG	CAT	TCC	CCT	1710
199	Arg	Ile	Pro	Pro	Ser	Gln	Phe	Ser	Pro	Ala	Gly	Ser	Leu	His	Ser	Pro	

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200				505				510				515					
202	GTG	GGA	GTT	TGC	AGC	AGC	ACA	GGA	AAT	AGC	CAT	AGT	TAT	ACC	AAC	AGC	1758
203	Val	Gly	Val	Cys	Ser	Ser	Thr	Gly	Asn	Ser	His	Ser	Tyr	Thr	Asn	Ser	
204				520				525				530					
206	TCC	CTC	AAT	GCA	CTT	CAG	GCC	CTC	AGC	GAG	GGG	CAC	GGG	GTC	TCA	TTA	1806
207	Ser	Leu	Asn	Ala	Leu	Gln	Ala	Leu	Ser	Glu	Gly	His	Gly	Val	Ser	Leu	
208				535				540				545					
210	GGG	TCA	TCG	TTG	GCT	TCA	CCA	GAC	CTA	AAA	ATG	GGC	AAT	TTG	CAA	AAC	1854
211	Gly	Ser	Ser	Leu	Ala	Ser	Pro	Asp	Leu	Lys	Met	Gly	Asn	Leu	Gln	Asn	
212				550				555				560					
214	TCC	CCA	GTT	AAT	ATG	AAT	CCT	CCC	CCA	CTC	AGC	AAG	ATG	GGA	AGC	TTG	1902
215	Ser	Pro	Val	Asn	Met	Asn	Pro	Pro	Pro	Leu	Ser	Lys	Met	Gly	Ser	Leu	
216	565						570				575				580		
218	GAC	TCA	AAA	GAC	TGT	TTT	GGA	CTA	TAT	GGG	GAG	CCC	TCT	GAA	GGT	ACA	1950
219	Asp	Ser	Lys	Asp	Cys	Phe	Gly	Leu	Tyr	Gly	Glu	Pro	Ser	Glu	Gly	Thr	
220				585				590				595					
222	ACT	GGA	CAA	GCA	GAG	AGC	AGC	TGC	CAT	CCT	GGA	GAG	CAA	AAG	GAA	ACA	1998
223	Thr	Gly	Gln	Ala	Glu	Ser	Ser	Cys	His	Pro	Gly	Glu	Gln	Lys	Glu	Thr	
224				600				605				610					
226	AAT	GAC	CCC	AAC	CTG	CCC	CCG	GCC	GTG	AGC	AGT	GAG	AGA	GCT	GAC	GGG	2046
227	Asn	Asp	Pro	Asn	Leu	Pro	Pro	Ala	Val	Ser	Ser	Glu	Arg	Ala	Asp	Gly	
228				615				620				625					
230	CAG	AGC	AGA	CTG	CAT	GAC	AGC	AAA	GGG	CAG	ACC	AAA	CTC	CTG	CAG	CTG	2094
231	Gln	Ser	Arg	Leu	His	Asp	Ser	Lys	Gly	Gln	Thr	Lys	Leu	Leu	Gln	Leu	
232				630				635				640					
234	CTG	ACC	ACC	AAA	TCT	GAT	CAG	ATG	GAG	CCC	TCG	CCC	TTA	GCC	AGC	TCT	2142
235	Leu	Thr	Thr	Lys	Ser	Asp	Gln	Met	Glu	Pro	Ser	Pro	Leu	Ala	Ser	Ser	
236	645						650				655				660		
238	TTG	TCG	GAT	ACA	AAC	AAA	GAC	TCC	ACA	GGT	AGC	TTG	CCT	GGT	TCT	GGG	2190
239	Leu	Ser	Asp	Thr	Asn	Lys	Asp	Ser	Thr	Gly	Ser	Leu	Pro	Gly	Ser	Gly	
240				665				670				675					
242	TCT	ACA	CAT	GGA	ACC	TCG	CTC	AAG	GAG	AAG	CAT	AAA	ATT	TTG	CAC	AGA	2238
243	Ser	Thr	His	Gly	Thr	Ser	Leu	Lys	Glu	Lys	His	Lys	Ile	Leu	His	Arg	
244				680				685				690					
246	CTC	TTG	CAG	GAC	AGC	AGT	TCC	CCT	GTG	GAC	TTG	GCC	AAG	TTA	ACA	GCA	2286
247	Leu	Leu	Gln	Asp	Ser	Ser	Ser	Pro	Val	Asp	Leu	Ala	Lys	Leu	Thr	Ala	
248				695				700				705					
250	GAA	GCC	ACA	GGC	AAA	GAC	CTG	AGC	CAG	GAG	TCC	AGC	AGC	ACA	GCT	CCT	2334
251	Glu	Ala	Thr	Gly	Lys	Asp	Leu	Ser	Gln	Glu	Ser	Ser	Ser	Thr	Ala	Pro	
252				710				715				720					
254	GGA	TCA	GAA	GTG	ACT	ATT	AAA	CAA	GAG	CCG	GTG	AGC	CCC	AAG	AAG	AAA	2382
255	Gly	Ser	Glu	Val	Thr	Ile	Lys	Gln	Glu	Pro	Val	Ser	Pro	Lys	Lys	Lys	
256	725						730				735				740		
258	GAG	AAT	GCA	CTA	CTT	CGC	TAT	TTG	CTA	GAT	AAA	GAT	GAT	ACT	AAA	GAT	2430
259	Glu	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Lys	Asp	Asp	Thr	Lys	Asp	
260				745				750				755					
262	ATT	GGT	TTA	CCA	GAA	ATA	ACC	CCC	AAA	CTT	GAG	AGA	CTG	GAC	AGT	AAG	2478
263	Ile	Gly	Leu	Pro	Glu	Ile	Thr	Pro	Lys	Leu	Glu	Arg	Leu	Asp	Ser	Lys	
264				760				765				770					

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266	ACA	GAT	CCT	GCC	AGT	AAC	ACA	AAA	TTA	ATA	GCA	ATG	AAA	ACT	GAG	AAG	2526
267	Thr	Asp	Pro	Ala	Ser	Asn	Thr	Lys	Leu	Ile	Ala	Met	Lys	Thr	Glu	Lys	
268			775					780					785				
270	GAG	GAG	ATG	AGC	TTT	GAG	CCT	GGT	GAC	CAG	CCT	GGC	AGT	GAG	CTG	GAC	2574
271	Glu	Glu	Met	Ser	Phe	Glu	Pro	Gly	Asp	Gln	Pro	Gly	Ser	Glu	Leu	Asp	
272			790				795					800					
274	AAC	TTG	GAG	GAG	ATT	TTG	GAT	GAT	TTG	CAG	AAT	AGT	CAA	TTA	CCA	CAG	2622
275	Asn	Leu	Glu	Glu	Ile	Leu	Asp	Asp	Leu	Gln	Asn	Ser	Gln	Leu	Pro	Gln	
276	805					810				815						820	
278	CTT	TTC	CCA	GAC	ACG	AGG	CCA	GGC	GCC	CCT	GCT	GGA	TCA	GTT	GAC	AAG	2670
279	Leu	Phe	Pro	Asp	Thr	Arg	Pro	Gly	Ala	Pro	Ala	Gly	Ser	Val	Asp	Lys	
280					825					830						835	
282	CAA	GCC	ATC	ATC	AAT	GAC	CTC	ATG	CAA	CTC	ACA	GCT	GAA	AAC	AGC	CCT	2718
283	Gln	Ala	Ile	Ile	Asn	Asp	Leu	Met	Gln	Leu	Thr	Ala	Glu	Asn	Ser	Pro	
284				840						845						850	
286	GTC	ACA	CCT	GTT	GGA	GCC	CAG	AAA	ACA	GCA	CTG	CGA	ATT	TCA	CAG	AGC	2766
287	Val	Thr	Pro	Val	Gly	Ala	Gln	Lys	Thr	Ala	Leu	Arg	Ile	Ser	Gln	Ser	
288			855					860					865				
290	ACT	TTT	AAT	AAC	CCA	CGA	CCA	GGG	CAA	CTG	GGC	AGG	TTA	TTG	CCA	AAC	2814
291	Thr	Phe	Asn	Asn	Pro	Arg	Pro	Gly	Gln	Leu	Gly	Arg	Leu	Leu	Pro	Asn	
292			870					875					880				
294	CAG	AAT	TTA	CCA	CTT	GAC	ATC	ACA	TTG	CAA	AGC	CCA	ACT	GGT	GCT	GGA	2862
295	Gln	Asn	Leu	Pro	Leu	Asp	Ile	Thr	Leu	Gln	Ser	Pro	Thr	Gly	Ala	Gly	
296	885					890					895					900	
298	CCT	TTC	CCA	CCA	ATC	AGA	AAC	AGT	AGT	CCC	TAC	TCA	GTG	ATA	CCT	CAG	2910
299	Pro	Phe	Pro	Pro	Ile	Arg	Asn	Ser	Ser	Pro	Tyr	Ser	Val	Ile	Pro	Gln	
300					905					910						915	
302	CCA	GGA	ATG	ATG	GGT	AAT	CAA	GGG	ATG	ATA	GGA	AAC	CAA	GGA	AAT	TTA	2958
303	Pro	Gly	Met	Met	Gly	Asn	Gln	Gly	Met	Ile	Gly	Asn	Gln	Gly	Asn	Leu	
304				920					925							930	
306	GGG	AAC	AGT	AGC	ACA	GGA	ATG	ATT	GGT	AAC	AGT	GCT	TCT	CGG	CCT	ACT	3006
307	Gly	Asn	Ser	Ser	Thr	Gly	Met	Ile	Gly	Asn	Ser	Ala	Ser	Arg	Pro	Thr	
308			935					940					945				
310	ATG	CCA	TCT	GGA	GAA	TGG	GCA	CCG	CAG	AGT	TCG	GCT	GTG	AGA	GTC	ACC	3054
311	Met	Pro	Ser	Gly	Glu	Trp	Ala	Pro	Gln	Ser	Ser	Ala	Val	Arg	Val	Thr	
312			950				955						960				
314	TGT	GCT	GCT	ACC	ACC	AGT	GCC	ATG	AAC	CGG	CCA	GTC	CAA	GGA	GGT	ATG	3102
315	Cys	Ala	Ala	Thr	Thr	Ser	Ala	Met	Asn	Arg	Pro	Val	Gln	Gly	Gly	Met	
316	965					970					975					980	
318	ATT	CGG	AAC	CCA	GCA	GCC	AGC	ATC	CCC	ATG	AGG	CCC	AGC	AGC	CAG	CCT	3150
319	Ile	Arg	Asn	Pro	Ala	Ala	Ser	Ile	Pro	Met	Arg	Pro	Ser	Ser	Gln	Pro	
320					985					990						995	
322	GGC	CAA	AGA	CAG	ACG	CTT	CAG	TCT	CAG	GTC	ATG	AAT	ATA	GGG	CCA	TCT	3198
323	Gly	Gln	Arg	Gln	Thr	Leu	Gln	Ser	Gln	Val	Met	Asn	Ile	Gly	Pro	Ser	
324				1000						1005						1010	
326	GAA	TTA	GAG	ATG	AAC	ATG	GGG	GGA	CCT	CAG	TAT	AGC	CAA	CAA	CAA	GCT	3246
327	Glu	Leu	Glu	Met	Asn	Met	Gly	Gly	Pro	Gln	Tyr	Ser	Gln	Gln	Gln	Ala	
328			1015							1020						1025	
330	CCT	CCA	AAT	CAG	ACT	GCC	CCA	TGG	CCT	GAA	AGC	ATC	CTG	CCT	ATA	GAC	3294

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09842256.txt

Output Set: N:\CRF3\12172001\I842256.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:790 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:1000 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:1021 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:1046 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:1064 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:1082 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:1100 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:1163 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:1172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1181 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1199 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14